

A. HANCOCK

[illegible]

R. Wilson

[illegible]

C JIMAC

[illegible]

9

16463 140 RRAAREASGFCVYVHDIYLAILELLKTYE---QVLTIRIRHKGDDVERAFTTIDIVTVFPNKT--GETFPPT 204
 H64N 832 RRAARETFPHFCFVYVSAVAANLLQQLSVS-K-IILTPVIRHKGDDVERAFTTIDIVTVFPNKT--GETFPPT 204
 16463 832 RRAARESTFPHFCFVYVSAVAANLLQQLSVS-K-VLITPVIRHKGDDVERAFTTIDIVTVFPNKT--GETFPPT 204
 H64N 835 RRAARESLGFCFVYVSAVAANLLQQLSVS-K-VLITPVIRHKGDDVERAFTTIDIVTVFPNKT--GETFPPT 204
 16463 835 RRAARESLGFCFVYVSAVAANLLQQLSVS-K-VLITPVIRHKGDDVERAFTTIDIVTVFPNKT--GETFPPT 204
 H64N 835 RRAARESLGFCFVYVSAVAANLLQQLSVS-K-VLITPVIRHKGDDVERAFTTIDIVTVFPNKT--GETFPPT 204
 16463 835 RRAARESLGFCFVYVSAVAANLLQQLSVS-K-VLITPVIRHKGDDVERAFTTIDIVTVFPNKT--GETFPPT 204
 H64N 835 RRAARESLGFCFVYVSAVAANLLQQLSVS-K-VLITPVIRHKGDDVERAFTTIDIVTVFPNKT--GETFPPT 204

Figure 2

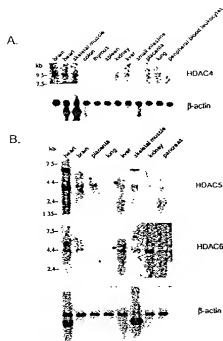
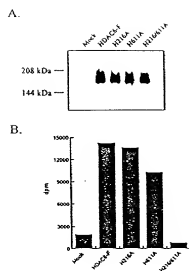


Figure 4



09800187.100904

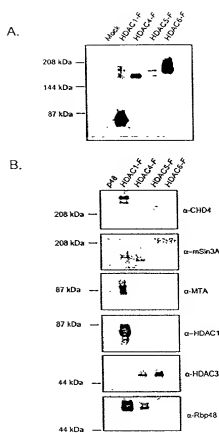


Figure 5

Figure 6

A.

HOMOLOGY REGIONS	INITIAL AA IN HDAC1	CONSENSUS SEQUENCES	EXCEPTIONS
1	99	DICITP (V) F NA	CLASS I CLASS II
2	134	NXXGCGEHA RPPG RHA	CLASS I CLASS II
3	148	SGIFVYCAKH GIFVYCAKH	CLASS I CLASS II
4	174	QDHHGGGV (V) QDHHGGGV Q	CLASS I CLASS II
5	193	VX T XSH VX (V) XSH	CLASS I CLASS II
6	225	HAP (M) XGGIDEX (V) Y NA	CLASS I CLASS II
7	258	KGGG Y KGGG (V) Y	CLASS I CLASS II

B.

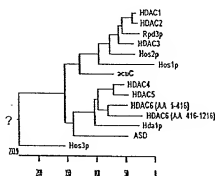


Figure 7

Figure 7A

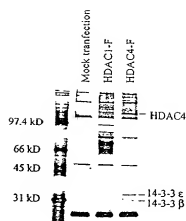


Figure 7B

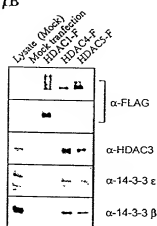


Figure 8

Figure 8A

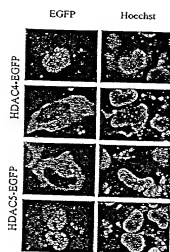


Figure 8B

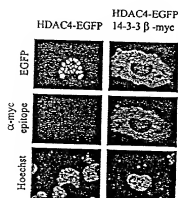


Figure 9A

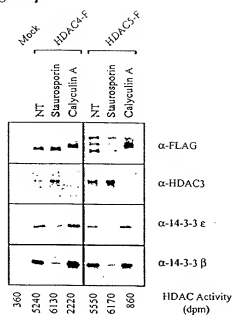


Figure 9

Figure 9B

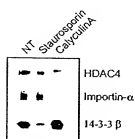
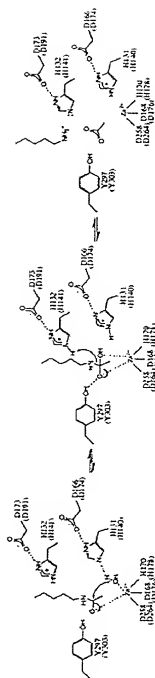


Figure 11



106001-28100860

Figure 12

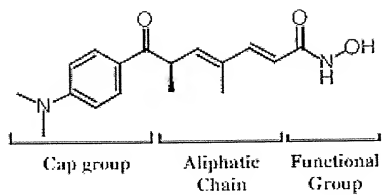


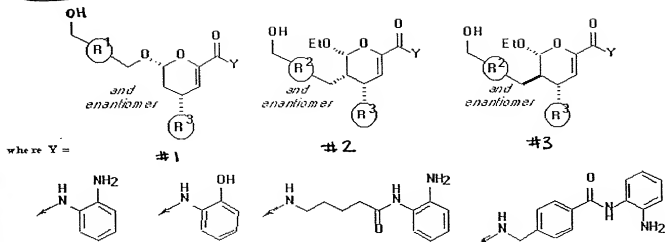
Figure 13

Residues on rim of channel										Residues in channel										
		1		2		3		4		5		6		7		8		9		
Class I	H101P	P	L	G	G	E	N	P	P	H101P	G	G	F	L	V	A	P	P	V	L
	H101M	P	L	G	G	E	N	P	P	H101M	G	G	F	L	V	A	P	P	V	L
	H101V	P	L	G	G	E	N	P	P	H101V	G	G	F	L	V	A	P	P	V	L
	H101I	P	M	G	G	E	N	P	P	H101I	G	G	F	L	V	A	P	P	V	L
	H101S	P	M	G	G	E	N	P	P	H101S	G	G	F	L	V	A	P	P	V	L
Class II	H101M	P	L	G	G	E	N	P	P	H101M	G	G	F	L	V	A	P	P	V	L
	H101V	P	L	G	G	E	N	P	P	H101V	G	G	F	L	V	A	P	P	V	L
	H101I	P	L	G	G	E	N	P	P	H101I	G	G	F	L	V	A	P	P	V	L
	H101S	P	L	G	G	E	N	P	P	H101S	G	G	F	L	V	A	P	P	V	L
	H101M	P	L	G	G	E	N	P	P	H101M	G	G	F	L	V	A	P	P	V	L
Class III	H101M	P	L	G	G	E	N	P	P	H101M	G	G	F	L	V	A	P	P	V	L
	H101V	P	L	G	G	E	N	P	P	H101V	G	G	F	L	V	A	P	P	V	L
	H101I	P	L	G	G	E	N	P	P	H101I	G	G	F	L	V	A	P	P	V	L
	H101S	P	L	G	G	E	N	P	P	H101S	G	G	F	L	V	A	P	P	V	L
	H101M	P	L	G	G	E	N	P	P	H101M	G	G	F	L	V	A	P	P	V	L
Class IV	H101M	P	L	G	G	E	N	P	P	H101M	G	G	F	L	V	A	P	P	V	L
	H101V	P	L	G	G	E	N	P	P	H101V	G	G	F	L	V	A	P	P	V	L
	H101I	P	L	G	G	E	N	P	P	H101I	G	G	F	L	V	A	P	P	V	L
	H101S	P	L	G	G	E	N	P	P	H101S	G	G	F	L	V	A	P	P	V	L
	H101M	P	L	G	G	E	N	P	P	H101M	G	G	F	L	V	A	P	P	V	L

Residues in active site									
		1		2		3		4	
Class I	H101P	P	L	G	G	E	N	P	P
	H101M	P	L	G	G	E	N	P	P
	H101V	P	L	G	G	E	N	P	P
	H101I	P	M	G	G	E	N	P	P
	H101S	P	M	G	G	E	N	P	P
Class II	H101M	P	L	G	G	E	N	P	P
	H101V	P	L	G	G	E	N	P	P
	H101I	P	L	G	G	E	N	P	P
	H101S	P	L	G	G	E	N	P	P
	H101M	P	L	G	G	E	N	P	P
Class III	H101M	P	L	G	G	E	N	P	P
	H101V	P	L	G	G	E	N	P	P
	H101I	P	L	G	G	E	N	P	P
	H101S	P	L	G	G	E	N	P	P
	H101M	P	L	G	G	E	N	P	P
Class IV	H101M	P	L	G	G	E	N	P	P
	H101V	P	L	G	G	E	N	P	P
	H101I	P	L	G	G	E	N	P	P
	H101S	P	L	G	G	E	N	P	P
	H101M	P	L	G	G	E	N	P	P

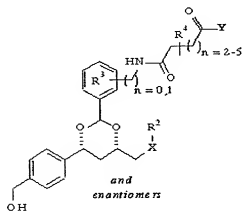
Figure 14

14A



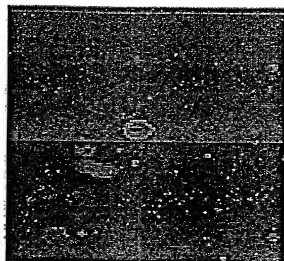
(4 R¹ groups + 2 R² groups) \leftrightarrow 10 R³ groups \leftrightarrow 2 (enantiomers) \leftrightarrow 4 amines = 640 compounds

14B



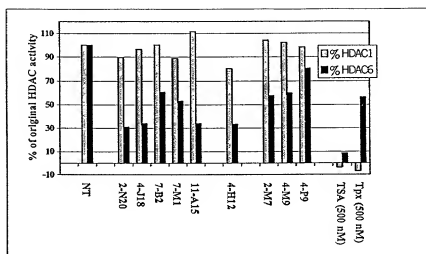
where Y = OH, NHOH, o-aminoaniline

Figure 15



09800187-100901

Figure 16



0960187.100901

Figure 17

